

X15815.ST25.txt
SEQUENCE LISTING

<110> Eli Lilly and Company
<120> Novel Proteins and Their Uses
<130> X-15815
<160> 24
<170> PatentIn version 3.2
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<212> DNA
<213> Homo sapiens

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X15815.ST25.txt

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 tgcagaactt ctccatgtca agcagcaggt gtcagcagga aaaagatcac aagcctgccca 1440
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 35 40 45
 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 50 55 60
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 65 70 75 80
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 85 90 95
 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
 100 105 110
 Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
 115 120 125
 Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
 130 135 140
 Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
 145 150 155 160
 Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
 165 170 175
 Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
 180 185 190

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Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
 195 200 205

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
 210 215 220

Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
 225 230 235 240

Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
 245 250 255

Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
 260 265 270

Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
 275 280 285

Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
 290 295 300

Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
 305 310 315 320

Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
 325 330 335

Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
 340 345 350

Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
 355 360 365

Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
 370 375 380

Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
 385 390 395 400

Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
 405 410 415

Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
 420 425 430

Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
 435 440 445

Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
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Asp Gly Cys Cys Ser Leu
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x15815.ST25.txt

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Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
 100 105 110

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
 115 120 125

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
 130 135 140

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
 145 150 155 160

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
 165 170 175

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
 180 185 190

X15815.ST25.txt

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
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Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
 210 215 220

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
 225 230 235 240

Gly Asp Ser Glu Gly Ala Thr Val Gln Gly Leu Ala Cys Pro Lys Ala
 245 250 255

Leu Ala Glu Gly Ser Gln Glu Asp His Cys Cys Ser Phe Phe Leu Glu
 260 265 270

Glu Met Phe Val Tyr Val Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser
 275 280 285

Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly
 290 295 300

Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu
 305 310 315 320

Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala
 325 330 335

Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe
 340 345 350

Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro
 355 360 365

Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu
 370 375 380

Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys
 385 390 395 400

Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys
 405 410 415

Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val
 420 425 430

Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser
 435 440 445

Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg
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X15815.ST25.txt

Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile
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Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His
 485 490 495

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Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys
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Cys Ser Leu
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35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
100 105 110

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
115 120 125

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
130 135 140

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
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X15815.ST25.txt

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
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Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
 180 185 190

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
 195 200 205

Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
 210 215 220

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
 225 230 235 240

Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
 245 250 255

Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
 260 265 270

Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
 275 280 285

Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
 290 295 300

Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Gly Ser Arg Arg Leu
 305 310 315 320

Pro Phe Leu Pro Pro His Tyr Cys Pro Pro Leu Arg Phe Leu Trp Phe
 325 330 335

Thr His Leu Lys Tyr Val Ser Ile Thr Gln Phe Val Thr Ser Leu Asn
 340 345 350

Phe Phe Lys Thr Ile Ala Glu Val Arg Ser Ser Leu Lys Ser Gly Arg
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Lys Arg Lys
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<213> Homo sapiens

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<223> LP394

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<400> 8

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Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
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Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
 100 105 110

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
 115 120 125

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
 130 135 140

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
 145 150 155 160

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
 165 170 175

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
 180 185 190

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
 195 200 205

Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
 210 215 220

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
 225 230 235 240

Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
 245 250 255

Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
 260 265 270

Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
 275 280 285

X15815.ST25.txt

Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
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Leu Lys Ser Gly Arg Lys Arg Lys
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 catgtcaagc agcaggtgtc agcaggaaaa agatcacaag cctgccacga tggctgctgc 1320

tccttgtagc ccacccatga gaagca X15815.ST25.txt

1346

<210> 10
 <211> 312
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(312)
 <223> LP395

<400> 10

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
 1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
 20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
 100 105 110

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
 115 120 125

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
 130 135 140

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
 145 150 155 160

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
 165 170 175

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
 180 185 190

Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
 195 200 205

X15815.ST25.txt

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
 210 215 220

Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
 225 230 235 240

Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
 245 250 255

Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
 260 265 270

Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
 275 280 285

Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Val Arg Ser Ser
 290 295 300

Leu Lys Ser Gly Arg Lys Arg Lys
 305 310

<210> 11
 <211> 1567
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(1567)
 <223> LP396

<400> 11
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 aatccccgga gacttgaggg acctccgagt agaacctgtt acaactagtg ttgcaacagg 180
 ggactattca attttgatga atgtaagctg ggtactccgg gcagatgcca gcatccgctt 240
 gttgaaggcc accaagattt gtgtgacggg caaaagcaac ttccagtcct acagctgtgt 300
 gaggtgcaat tacacagagg ctttccagac tcagaccaga ccctctggtg gtaaattggac 360
 attttcttac atcgggttcc ctgtagagct gaacacagtc tatttcattg gggcccataa 420
 tattcctaata gcaaatatga atgaagatgg cccttccatg tctgtgaatt tcacctcacc 480
 aggctgccta gaccacataa tgaaatataa aaaaaagtgt gtcaaggccg gaagcctgtg 540
 ggatccgaac atcactgctt gtaagaagaa tgaggagaca gtagaagtga acttcacaac 600
 cactcccctg ggaaacagat acatggctct tatccaacac agcactatca tcgggttttc 660
 tcagggtgtt gagccacacc agaagaaaca aacgcgagct tcagtgggtga ttccagtgc 720
 tggggatagt gaaggtgcta cggtgcagat gtgtgaccaa ggggaaaatg tgcattgacaa 780
 cactagagct gactccatat tttcctactt gtggcagcga ctgcatccga cataaaggaa 840

X15815.ST25.txt

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cagttgtgct ctgcccacaa acaggcgctcc ctttccctct ggataacaac aaaagcaagc 900
cgggaggctg gctgcctctc ctctgctgt ctctgctggt ggccacatgg gtgctggtgg 960
cagggatcta tctaattgtg aggcacgaaa ggatcaagaa gacttccctt tctaccacca 1020
cactactgcc cccattaag gttcttgtgg ttaccatc tgaaatatgt ttccatcaca 1080
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actttagaga gattgataca aaagacgatt acaatgctct cagtgtctgc cccaagtacc 1440
acctcatgaa ggatgccact gctttctgtg cagaacttct ccatgtcaag cagcaggtgt 1500
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agaagca 1567

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<210> 12
<211> 277
<212> PRT
<213> Homo sapiens

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<220>
<221> MISC_FEATURE
<222> (1)..(277)
<223> LP396

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<400> 12

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Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15

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Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30

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```

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

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Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

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Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

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Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

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Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
100 105 110

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X15815.ST25.txt

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
 115 120 125

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
 130 135 140

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
 145 150 155 160

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
 165 170 175

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
 180 185 190

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
 195 200 205

Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
 210 215 220

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
 225 230 235 240

Gly Asp Ser Glu Gly Ala Thr Val Gln Met Cys Asp Gln Gly Glu Asn
 245 250 255

Val His Asp Asn Thr Arg Ala Asp Ser Ile Phe Ser Tyr Leu Trp Gln
 260 265 270

Arg Leu His Pro Thr
 275

<210> 13
 <211> 1352
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1352)
 <223> LP397

<400> 13
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 aatcccggga gacttgaggg acctccgagt agaacctgtt acaactagtg ttgcaacagg 180
 ggactattca attttgatga atgtaagctg ggtactccgg gcagatgcca gcatccgctt 240
 gttgaaggcc accaagattt gtgtgacggg caaaagcaac ttccagtcct acagctgtgt 300
 gaggtgcaat tacacagagg ccttccagac tcagaccaga ccctctggtg gtaaattggac 360

X15815.ST25.txt

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aggctgccta gaccacataa tgaaatataa aaaaaagtgt gtcaaggccg gaagcctgtg 540
ggatccgaac atcactgctt gtaagaagaa tgaggagaca gtagaagtga acttcacaac 600
cactcccctg ggaaacagat acatggctct tatccaacac agcactatca tcgggttttc 660
tcagggtgttt gagacaaaag caagccggga ggctggctgc ctctcctcct gctgtctctg 720
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gctctcagtg tctgccccaa gtaccacctc atgaaggatg ccactgcttt ctgtgcagaa 1260
cttctccatg tcaagcagca ggtgtcagca ggaaaaagat cacaagcctg ccacgatggc 1320
tgctgctcct tgtagccac ccatgagaag ca 1352

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<210> 14
 <211> 252
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(252)
 <223> LP397

<400> 14

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
 1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
 20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 65 70 75 80

X15815.ST25.txt

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
100 105 110

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
115 120 125

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
130 135 140

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
145 150 155 160

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
165 170 175

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
180 185 190

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
195 200 205

Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
210 215 220

Thr Lys Ala Ser Arg Glu Ala Gly Cys Leu Ser Ser Cys Cys Leu Cys
225 230 235 240

Trp Trp Pro His Gly Cys Trp Trp Gln Gly Ser Ile
245 250

<210> 15
<211> 1399
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(1399)
<223> LP398

<400> 15
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aatcccggga gacttgaggg acctccgagt agaacctgtt acaactagtg ttgcaacagg 180
ggactattca attttgatga atgtaagctg ggtactccgg gcagatgtgg acattttcct 240
acatcggtt ccctgtagag ctgaacacag tctatttcat tggggcccat aatattccta 300
atgcaaatat gaatgaagat ggcccttcca tgtctgtgaa ttccacctca ccaggctgcc 360

X15815.ST25.txt

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tagaccacat aatgaaatat aaaaaaaagt gtgtcaaggc cggaagcctg tgggatccga 420
acatcactgc ttgtaagaag aatgaggaga cagtagaagt gaacttcaca accactcccc 480
tgggaaacag atacatggct cttatccaac acagcactat catcggggtt tctcagggtg 540
ttgagccaca ccagaagaaa caaacgcgag cttcagtggt gattccagtg actggggata 600
gtgaagggtgc tacggtgcag ctgactccat attttccctac ttgtggcagc gactgcatcc 660
gacataaagg aacagttgtg ctctgcccac aaacaggcgt ccctttccct ctggataaca 720
acaaaagcaa gccgggaggc tggctgcctc tcctcctgct gtctctgctg gtggccacat 780
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tcatccttga aaagtggcag aaaaagaaaa tagcagagat ggggtccagt cagtggcttg 1020
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gccccaaagta ccacctcatg aaggatgcc aagccttgcca tgcagaactt ctccatgtca 1320
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agccccacca tgagaagca 1399

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<210> 16
 <211> 96
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(96)
 <223> LP398

<400> 16

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Val Asp Ile Phe Leu
65 70 75 80

X15815.ST25.txt

His Arg Leu Pro Cys Arg Ala Glu His Ser Leu Phe His Trp Gly Pro
 85 90 95

<210> 17
 <211> 1081
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1081)
 <223> LP399

<400> 17
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 aatccccgga gacttgaggg acctccgagt agaacctgtt acaactagtg ttgcaacagg 180
 ggactattca attttgatga atgtaagctg ggtactccgg gcagatgcca caccagaaga 240
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 agctgactcc atattttcct acttgtggca gcgactgcat ccgacataaa ggaacagttg 360
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 cagacaaagt cgtcttcctt ctttccaatg acgtcaacag tgtgtgcat ggtacctgtg 780
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 gagagattga taaaaagac gattacaatg ctctcagtg ctgccccaaag taccacctca 960
 tgaaggatgc cactgcttct tgtgcagaac ttctccatgt caagcagcag gtgtcagcag 1020
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 a 1081

<210> 18
 <211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(93)
 <223> LP399

X15815.ST25.txt

<400> 18

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
 1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
 20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Thr Pro Glu Glu
 65 70 75 80

Thr Asn Ala Ser Phe Ser Gly Asp Ser Ser Asp Trp Gly
 85 90

<210> 19

<211> 940

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(940)

<223> LP417

<400> 19

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 tgattccagt gactggggat agtgaaggtg ctacggtgca gctgactcca tattttccta 180
 cttgtggcag cgactgcatc cgacataaag gaacagttgt gctctgcca caaacaggcg 240
 tccctttccc tctggataac aacaaaagca agccgggagg ctggctgcct ctctctctgc 300
 tgtctctgct ggtggccaca tgggtgctgg tggcagggat ctatctaata tggaggcacg 360
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 gtgagaactc tcaagacctc tttccccttg cttttaacct tttctgcagt gatctaagaa 720
 gccagattca tctgcacaaa tacgtggtgg tctacttttag agagattgat acaaaagacg 780
 attacaatgc tctcagtgtc tgcccgaagt accacctcat gaaggatgcc actgctttct 840
 gtgcagaact tctccatgtc aagcagcagg tgtcagcagg aaaaagatca caagcctgcc 900

X15815.ST25.txt

acgatggctg ctgctccttg tagccccaccc atgagaagca

940

<210> 20
 <211> 46
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(46)
 <223> LP417

<400> 20

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
 1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Ala Thr Pro Glu
 20 25 30

Glu Thr Asn Ala Ser Phe Ser Gly Asp Ser Ser Asp Trp Gly
 35 40 45

<210> 21
 <211> 1352
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1352)
 <223> LP418

<400> 21
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 aatccccgga gacttgaggg acctccgagt agaacctgtt acaactagtg ttgcaacagg 180
 ggactattca attttgatga atgtaagctg ggtactccgg gcagatgcca gcatccgctt 240
 gttgaaggcc accaagattt gtgtgacggg caaaagcaac ttccagtcct acagctgtgt 300
 gaggtgcaat tacacagagg ccttccagac tcagaccaga ccctctggtg gtaaagaagc 360
 ctgtgggatc cgaacatcac tgcttgtaag aagaatgagg agacagtaga agtgaacttc 420
 acaaccactc ccctgggaaa cagatacatg gctcttatcc aacacagcac tatcatcggg 480
 ttttctcagg tgtttgagcc acaccagaag aaacaaacgc gagcttcagt ggtgattcca 540
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 agcgactgca tccgacataa aggaacagtt gtgctctgcc cacaacagg cgtccctttc 660
 cctctggata acaacaaaag caagccggga ggctggctgc ctctcctcct gctgtctctg 720
 ctggtggcca catgggtgct ggtggcaggg atctatctaa tgtggaggca cgaaaggatc 780
 aagaagactt ctttttctac caccacacta ctgcccccca ttaaggttct tgtggtttac 840

X15815.ST25.txt

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gctctcagtg tctgccccaa gtaccacctc atgaaggatg ccaactgcttt ctgtgcagaa 1260
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<210> 22
 <211> 135
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(135)
 <223> LP418

<400> 22

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
100 105 110

Arg Pro Ser Gly Gly Lys Glu Ala Cys Gly Ile Arg Thr Ser Leu Leu
115 120 125

Val Arg Arg Met Arg Arg Gln
130 135

x15815.ST25.txt

<210> 23
 <211> 1210
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1210)
 <223> LP419

<400> 23
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 tgaacacagt ctatttcatt ggggccata atattcctaa tgcaaatatg aatgaagatg 180
 gcccttccat gtctgtgaat ttcacctcac caggaagcct gtgggatccg aacatcactg 240
 cttgtaagaa gaatgaggag acagtagaag tgaacttcac aaccactccc ctgggaaaca 300
 gatacatggc tcttatccaa cacagcacta tcatcgggtt ttctcagggtg tttgagccac 360
 accagaagaa acaaacgcga gcttcagtgg tgattccagt gactggggat agtgaagggtg 420
 ctacgggtgca gctgactcca tattttccta cttgtggcag cgactgcata cgacataaag 480
 gaacagttgt gctctgcccc caaacaggcg tccctttccc tctggataac aacaaaagca 540
 agccgggagg ctggctgcct ctctcctgc tgtctctgct ggtggccaca tgggtgctgg 600
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X15815.ST25.txt

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Pro